

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 16:27:37 ; Search time 88.01 Seconds
(without alignments)
221.574 Million cell updates/sec

Title: US-09-534-229C-1
Perfect score: 1362
Sequence: 1 MARFAALAVCAAAALLAVAA.....MLGTATGNNLDCYTQRFAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

30	724	53.2	335	2	T03239	able chitinase
31	723	53.1	320	2	S59947	itnase (EC 3.2.
32	723	53.1	324	2	T10802	itnase (EC 3.2.
33	721.5	53.0	318	2	S14948	chitinase (EC 3.2.
34	721.5	53.0	327	2	T09687	chitinase (EC 3.2.
35	711.5	52.2	327	1	JQ0965	chitinase (EC 3.2.
36	711	52.2	302	2	T10810	chitinase (EC 3.2.
37	709	52.1	328	1	S05426	chitinase (EC 3.2.
38	708	52.0	334	2	S20982	chitinase class 1
39	707.5	51.9	321	2	S57482	chitinase (EC 3.2.
40	705.5	51.8	324	2	S20981	chitinase (EC 3.2.
41	705	51.8	316	2	S65020	chitinase (EC 3.2.
42	705	51.8	318	2	S65019	chitinase (EC 3.2.
43	701	51.5	329	2	S08627	chitinase (EC 3.2.
44	699	51.3	318	2	S43317	chitinase (EC 3.2.
45	699	51.3	324	2	S56694	chitinase (EC 3.2.

ALIGNMENTS

RESULT 1

S48847
chitinase (EC 3.2.1.14) cht2a precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S48847
R;Byrgelsson, T.; Collinge, D.B.; Green, B.; Gumnesson, P.O.; Kragh, K.; Thordal-C
submitted to the EMBL Data Library, March 1994
A;Description: Purification, characterization and cDNA sequence of a basic chitinase.
A;Reference number: S48847
A;Accession: S48847
A;Molecule type: mRNA
A;Residues: 1-256 <BRY>
A;Cross-references: EMBL:X78671; NID:g563486; PIDN:CAA55344.1; PID:g563487
C;Genetics:
A;Gene: cht2a
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-256/Product: chitinase cht2a #status predicted <MAP>
F;31-255/Domain: plant chitinase homology <PCH>

Query Match 97.9%; Score 1334; DB 2; Length 256;
Best Local Similarity 98.4%; Pred. No. 2e-108;
Matches 252; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	MARFAALAVCAAAALLAVAAAGGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAF	60
Db	1	MARPAALAVCAAAALLAVAVGGAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAF	60
QY	61	IAAANTFPFGTGSADDIKRDLAAFFGOTSHETTGTRGAADQFOWGYCFKEISKATS	120
Db	61	IAAANTFPFGTGSADDIKRDLAAFFGOTSHETTGTRGAADQFOWGYCFKEISKATS	120
QY	121	PPYGRGPQLTGRSNYDLAIGRAIGKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPS	180
Db	121	PPYGRGPQLTGRSNYDLAIGRAIGKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPS	180
QY	181	HNVALRRWTPTAADAAGRVPGYGVITNTINGGLECGMGRNDANVDRIYTRYCGMLGT	240
Db	181	HNVALRRWTPTAADAAGRVPGYGVITNTINGGLECGMGRNDANVDRIYTRYCGMLGT	240
QY	241	ATGNNLDCYTQRFAS	256
Db	241	ATGNNLDCYTQRFAS	256

RESULT 2

S48848
chitinase (EC 3.2.1.14) cht2b precursor - barley
C;Species: Hordeum vulgare (barley)

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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:32:12 ; Search time 88.01 Seconds
(without alignments)
276.101 Million cell updates/sec

Title: US-09-534-229C-3
Perfect score: 1765
Sequence: 1 MRGVVVVWMLAAFAVSAHA.....DLLGVSYGDNLDYCNORPFA 319
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

30	1168.5	66.2	327	1	J00965	tinase (EC 3.2.
31	1167.5	66.1	329	2	T06999	tinase (EC 3.2.
32	1162	65.8	321	2	S57482	chitinase class 1
33	1156	65.5	308	2	JC2253	chitinase (EC 3.2.
34	1154.5	65.4	302	2	T10810	chitinase (EC 3.2.
35	1140	64.6	243	2	JN0884	chitinase (EC 3.2.
36	1125	63.7	265	2	A38664	chitinase (EC 3.2.
37	1120	63.5	243	2	JC5918	chitinase (EC 3.2.
38	1099.5	62.3	318	2	T03036	chitinase (EC 3.2.
39	1071	60.7	263	2	S72528	chitinase (EC 3.2.
40	1045	59.2	264	2	S26625	chitinase (EC 3.2.
41	1022.5	57.9	340	2	S48030	probable chitinase
42	1012	57.3	263	2	S69184	chitinase (EC 3.2.
43	1004	56.9	246	2	S37341	chitinase (EC 3.2.
44	993	56.3	336	1	S18750	chitinase (EC 3.2.
45	966	54.7	275	2	T03032	chitinase (EC 3.2.

ALIGNMENTS

RESULT 1

S38670
chitinase (EC 3.2.1.14) - wheat
C:Species: Triticum aestivum (Common wheat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Jun-1999
C:Accession: S38670
R:Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reissner, H.J.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38670
A:Accession: S38670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <Lia>
A:Cross-references: EMBL:X76041; NID:g416028; PIDN:CAA53626.1; PID:g416029
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homolog:
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-320/Domain: plant chitinase homology <PCH>

Query Match 96.1%; Score 1696.5; DB 2; Length 320;

Best Local Similarity 95.3%; Pred. No. 6.8e-119;

Matches 305; Conservative 9; Mismatches 5; Indels. 1; Gaps 1;

Qy	1	MRGVVVWMLAAFAVSAHAECQSQAGATCPNCLCCSKFGFCGTTSDYCGTGCSQCN	60
Db	1	MRGVVVWMLAAFAVSAHAECQSQAGATCPNCLCCSKFGFCGTTSDYCGTGCSQCN	60
Qy	61	GCS-GGTPVPVPTPSGGVSSIIISQSLFDQMLLRNDAAACAKFGFNYGAFVAAANSFSG	119
Db	61	GCSGGTVPVPTPTGGGVSSIIISQSLFDQMLLRNDAAACAKFGFNYGAFVAAANSFSG	120
Qy	120	FATTGSTDVKKREVAFLAQTSHETGGTAPDGPYSGYCFNQRGATSDYCTPSSOW	179
Db	121	FATTGADYRKEVAFLAQTSHETGGTAPDGPYSGYCFNQRGAASDYCPNSOW	180
Qy	180	PCAPGKYGFRGPIQISHNINYPAGQAIGTDLNNDLVASDATVSKTALFWMTPOS	239
Db	181	PCAPGKYGFRGPIQISYNINYPAGRAIGTDLNNDLVATDATVSKTALFWMTPOS	240
Qy	240	PKPSSHVDITGRWSPSGADQAAGRVPGYGVITNIINGLECGRGDGRVADRIGFYKRYC	299
Db	241	PKPSSHVDITGRWSPSGADQAAGRVPGYGVITNIINGLECGRGDGRVADRIGFYKRYC	300
Qy	300	DLLGVSYGDNLDYCNORPFA	319
Db	301	DLLGVSYGDNLDYCNORPFA	320

RESULT 2

JC2071
chitinase (EC 3.2.1.14) a - rye

CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat P1173438 (of high snow mould resistance). The genes are
 CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.
 XX
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1792; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2.6e-144;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTLRACATAVLAVLAAAVTATAEQCSQAGGAKADCLCCSFGCGTTSYDYGCP 60
 Db 1 mstlracatavlavlaaavtataeqcsqaggaakadclccsfgcgttsdydycp 60
 QY 61 RCQSQCCTCGCGGGGVASIVSRDLFERLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
 Db 61 rcqsqctcgcggggvasivsrdlferllhrndaacrlargfyttydaflaaagafpafgt 120
 121 TGDLDTRKREVAFFGOTSHETTGWPTAPDGFPSWGCYCFKQSGSPSYCDOSADWPCA 180
 Db 121 tgdldtrkrevaaffgotshetggwptapgpfswgcyfkwsgspssycdgsadwpca 180
 QY 181 PGQYGRGPIQLTHNYNYPAGRAIGVDLLNPNDLVATDPTVAFKTAIWFWMTTOSNKP 240
 Db 181 pgqygrgpiqlthnynypagraigvdlldnnpdlvatdptvafktaiwfwmttqsnkp 240
 QY 241 SCHDVITGLWPTARSAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDIF 300
 Db 241 schdvtglwptarsaagrpgygvitnvningiecgmgqndkvadrifgfykrycdif 300
 QY 301 GIGYGNLDCYNOLSFNVLAAQ 323
 Db 301 gigygnldcynqlsfavglaaq 323

RESULT 2
 ID AAB11489
 XX AAB11489 standard; protein; 319 AA.
 AC AAB11489;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Wheat chitinase protein homologous to spring wheat chitinase.
 XX
 KW Wheat; chitinase; low temperature expression; hardened; plant;
 XX snow mould resistance; psychophilic plant pathogen; spring wheat.
 OS Triticum aestivum.
 XX
 PN JP2000270866-A.
 XX
 PD 03-OCT-2000.
 XX
 PF 25-MAR-1999; 95JP-0081694.
 XX
 PR 25-MAR-1999; 95JP-0081694.
 XX
 XX (HOKK-) HOKKAIDO NOGHO SHIKENBACHO.
 PA
 XX WPI; 2001-027417/04.
 DR
 XX New low temperature expression chitinase gene for producing a plant
 PT grade highly resistant to psychophilic plant pathogenic microbes -
 XX
 PS Claim 7; Fig 3; 1lpp; Japanese.
 XX

CC This invention describes novel wheat chitinase genes. The invention also
 CC describes a method for the isolation of a low temperature expression
 CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat P1173438 (of high snow mould resistance). The genes are

Tue M

CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.
 XX
 SQ Sequence 319 AA;

Query Match 72.2%; Score 1294.5; DB 22; Length 319;
 Best Local Similarity 71.0%; Pred. No. 4.5e-102;
 Matches 223; Conservative 34; Mismatches 48; Indels 9; Gaps 1;
 QY 12 VLAVLAAAVTATAEQCSQAGGAKADCLCCSFGCGTTSYDYGPRCQSOCTCGCG 71
 Db 5 vvvamlaaafavsaahaeqcsqaggaatcpnclccsfgcgttsdydycgqngcsg 64
 QY 72 G-----GGGVASIVSRDLFERLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 122
 Db 65 gtpvptpsggvssllsqslfdqmlhrndaacrlargfytydaflaaagafpafgt 124
 QY 123 DLDTRKREVAFFGOTSHETTGWPTAPDGFPSWGCYCFKQSGSPSYCDOSADWPCA 182
 Db 125 stdvkkrevaaffgotshetggwptapgpfswgcyfkwsgspssycdgsadwpca 184
 QY 183 KOYGRGPIQLTHNYNYPAGRAIGVDLLNPNDLVATDPTVAFKTAIWFWMTTOSNKP 242
 Db 185 kkyfgrgpiqlthnynypagraigvdlldnnpdlvatdptvafktaiwfwmtqspkps 244
 QY 243 HDVITGLWPTARSAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDIF 302
 Db 245 hdvitgrwspgadqagrpgygvitnvningiecgmgqndkvadrifgfykrycdilgv 304
 QY 303 GYGNLDCYNOLSF 316
 Db 305 sygndldcynqrpf 318

RESULT 3
 ID AAW98079
 XX AAW98079 standard; Protein; 318 AA.
 AC AAW98079;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Rye chitinase-like protein CHT9 preprotein.
 XX
 KW CHT9; chitinase-like protein; antifreeze protein; AFP;
 XX winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.
 XX
 OS Secale cereale.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 FT Protein 21..318
 FT /note= "mature protein, also claimed in Claim 10"
 XX
 PN WO9906565-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-CA00745.
 XX
 PR 31-JUL-1997; 97US-0903872.
 XX
 PA (ICEB-) ICE BIOTECH INC.
 XX
 PI Griffith M, Hew C, Moffatt B, Xiong F;
 XX
 DR WPI; 1999-153795/13.
 DR N-PSDB; AAX24889.
 XX
 PT New nucleic acid encoding antifreeze polypeptides from plants -

Abstract